STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/575,096*
Source: *IFWP*
Date Processed by STIC: *4/24/06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/575,096_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 ____ Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)

Sequence(s) ____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFWP

RAW SEQUENCE LISTING   DATE: 04/24/2006
PATENT APPLICATION: US/10/575,096   TIME: 16:09:54

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

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    3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
    5 <120> TITLE OF INVENTION: Process for the antibody composition using RNA
which inhibits a function
    6         of a1,6-fucosyltransferase
    8 <130> FILE REFERENCE: 11621WO1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/575,096
C--> 10 <141> CURRENT FILING DATE: 2006-04-10
   10 <150> PRIOR APPLICATION NUMBER: P2003-350167
   11 <151> PRIOR FILING DATE: 2003-10-09
E--> 13 <160> NUMBER OF SEQ ID NOS: 35
   15 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

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  266 <210> SEQ ID NO: 5
  267 <211> LENGTH: 575
  268 <212> TYPE: PRT
  269 <213> ORGANISM: Cricetulus griseus
  271 <400> SEQUENCE: 5
  272 Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
  273   1               5              10                  15
  275 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
  276               20              25                  30
  278 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
  279           35              40                  45
  281 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
  282       50              55                  60
  284 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
  285  65              70                  75                  80
  287 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
  288               85              90                  95
  290 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Asp Leu Gly Lys Asp His
  291              100             105                 110
  293 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
  294             115             120                 125
  296 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Lys Leu Glu Gly Asn Glu
  297         130             135                 140
  299 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
  300 145             150                 155                 160
  302 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
  303             165             170                 175
  305 Gly Glu Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
  306             180             185                 190
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RAW SEQUENCE LISTING   DATE: 04/24/2006
PATENT APPLICATION: US/10/575,096   TIME: 16:09:54

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

308 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
309   195   200   205
311 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
312   210   215   220
314 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
315 225   230   235   240
317 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
318   245   250   255
320 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
321   260   265   270
323 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
324   275   280   285
326 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
327   290   295   300
329 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
330 305   310   315   320
332 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
333   325   330   335
335 Arg Pro Gln Pro Trp Leu Glu Arg Glu Ile Glu Glu Thr Thr Lys Lys
336   340   345   350
338 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
339   355   360   365
341 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
342   370   375   380
344 His Val Glu Glu His Phe Gln Leu Leu Glu Arg Arg Met Lys Val Asp
345 385   390   395   400
347 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
348   405   410   415
350 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
351   420   425   430
353 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
354   435   440   445
356 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
357   450   455   460
359 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
360 465   470   475   480
362 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
363   485   490   495
365 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
366   500   505   510
368 His Gln Pro Arg Thr Lys Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
369   515   520   525
371 Ile Gly Val Ala Gly Asn His Trp Asn Gly Tyr Ser Lys Gly Val Asn
372   530   535   540
374 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
375 545   550   555   560
377 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
E--> 378   565   570   *575 ← insert*
381 <210> SEQ ID NO: 6

P.4

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382 <211> LENGTH: 575
383 <212> TYPE: PRT
384 <213> ORGANISM: Mus musculus
386 <400> SEQUENCE: 6
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388   1               5                  10                  15
390 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
391                  20                  25                  30
393 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
394              35                  40                  45
396 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
397          50                  55                  60
399 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
400  65                  70                  75                  80
402 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
403                  85                  90                  95
405 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
406             100                 105                 110
408 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
409         115                 120                 125
411 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
412         130                 135                 140
414 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
415 145                 150                 155                 160
417 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
418             165                 170                 175
420 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
421             180                 185                 190
423 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
424         195                 200                 205
426 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
427     210                 215                 220
429 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
430 225                 230                 235                 240
432 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
433             245                 250                 255
435 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
436             260                 265                 270
438 Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
439         275                 280                 285
441 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
442     290                 295                 300
444 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
445 305                 310                 315                 320
447 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
448             325                 330                 335
450 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
451             340                 345                 350
453 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
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Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

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454          355              360              365
456 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
457     370              375              380
459 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
460 385              390              395              400
462 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu
463              405              410              415
465 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
466              420              425              430
468 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
469     435              440              445
471 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
472     450              455              460
474 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
475 465              470              475              480
477 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
478              485              490              495
480 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
481              500              505              510
483 His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
484     515              520              525
486 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
487     530              535              540
489 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
490 545              550              555              560
492 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
493              565              570              575
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496 <210> SEQ ID NO: 7
497 <211> LENGTH: 575
498 <212> TYPE: PRT
499 <214> Rattus norvegicus

501 <400> SEQUENCE: 7
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503 1              5              10              15
505 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
506              20              25              30
508 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
509              35              40              45
511 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
512     50              55              60
514 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
515 65              70              75              80
517 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
518              85              90              95
520 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
521              100              105              110
523 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
524              115              120              125
```

```
526 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
527     130                 135                 140
529 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
530 145                 150                 155                 160
532 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
533                 165                 170                 175
535 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
536             180                 185                 190
538 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
539             195                 200                 205
541 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
542     210                 215                 220
544 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
545 225                 230                 235                 240
547 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
548                 245                 250                 255
550 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
551             260                 265                 270
553 Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
554         275                 280                 285
556 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
557     290                 295                 300
559 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
560 305                 310                 315                 320
562 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
563             325                 330                 335
565 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
566             340                 345                 350
568 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
569         355                 360                 365
571 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
572     370                 375                 380
574 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
575 385                 390                 395                 400
577 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
578             405                 410                 415
580 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
581             420                 425                 430
583 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
584         435                 440                 445
586 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
587     450                 455                 460
589 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
590 465                 470                 475                 480
592 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
593             485                 490                 495
595 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
596             500                 505                 510
598 His Lys Pro Arg Thr Asp Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
```

```
599          515                 520                 525
601 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn
602      530                 535        .          540
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605 545              550                 555                 560
607 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
E--> 608              565                 570
611 <210> SEQ ID NO: 8
612 <211> LENGTH: 575
613 <212> TYPE: PRT
E--> 614 <213> Homo Sapience
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621              20                 25                  30
623 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
624          35                 40                  45
626 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
627      50                 55                  60
629 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile
630  65                 70                 75                  80
632 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
633              85                 90                  95
635 Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His
636              100                105                 110
638 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
639          115                120                 125
641 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
642      130                135                140
644 Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu
645 145              150                155                 160
647 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
648              165                170                175
650 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
651              180                185                190
653 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
654          195                200                205
656 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
657      210                215                220
659 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
660 225              230                235                 240
662 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
664              245                250                 255
666 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile
667              260                265                 270
669 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
670          275                280                 285
```

Handwritten annotations: "<213" ; "575 ← insert" ; "same err in sequence 4" ; "Sapiens" ; "see p. 7"

RAW SEQUENCE LISTING   DATE: 04/24/2006
PATENT APPLICATION: US/10/575,096   TIME: 16:09:54

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

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672 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
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675 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
676 305             310             315                 320
678 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
679             325             330                 335
681 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
682             340             345             350
684 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
685         355             360             365
687 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
688     370             375             380
690 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
691 385             390             395                 400
693 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
694             405             410             415
696 Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
697         420             425             430
699 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
700         435             440             445
702 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
703     450             455             460
705 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
706 465             470             475                 480
708 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
709             485             490                 495
711 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala
712         500             505             510
714 His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile
715     515             520             525
717 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn
718     530             535             540
720 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
721 545             550             555                 560
723 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
E--> 724             565             570
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575 ← insert [handwritten]

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            1   ±   `    5   -5    `   10   -10-

misaligned numbers

```
<400> 53
gaa ttc ggc atc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt   48
            Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu
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resolyried numbers

<210> 54   *last sequence in file*
<211> 199
<212> PRT
<213> Homo sapiens

<400> 54

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            20                  25                  30
Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
            35                  40                  45
Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
     50                  55                  60
Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65                  70                  75                  80
Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
            85                  90                  95
Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
            100                 105                 110
Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
            115                 120                 125
His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
     130                 135                 140
Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145                 150                 155                 160
Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
            165                 170                 175
Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
            180                 185                 190
Gly His His His His His His
            195
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VERIFICATION SUMMARY   DATE: 04/24/2006
PATENT APPLICATION: **US/10/575,096**   TIME: 16:09:55

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\04242006\J575096.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:378 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:493 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:499 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:501 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:608 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:614 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:616 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:724 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:1044 M:283 W: Missing Blank Line separator, <220> field identifier
L:1045 M:283 W: Missing Blank Line separator, <400> field identifier
L:1114 M:283 W: Missing Blank Line separator, <220> field identifier
L:1241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1361 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1388 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:13 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (35) Counted
(54)